

FtsZ-m12 consensus2 Map.MPD (1 > 1423) Site and Sequence

Enzymes : 50 of 502 enzymes (Filtered)

Settings : Circular, Certain Sites Only, Standard Genetic Code

EcoR V

GATGGCGATATCCGCGATGAAGCTGCGCGATGGCGCTGCTACGTGCGCCGCGAGACCTCCGAGTCCGCCACTCA 75

CTACCCCTATAGGCGTACTTTGACGCGCGCTACCGGAGCATGCACGGGCGGTCTGGAGGCTCAGGCGGTGAGT

Met Ala Ile Ser Arg Met Lys Ala Ala Met Ala Leu Leu Arg Ala Arg Gln Thr Ser Gln Ala Thr Gln

Pst I

Pvu II

ACACCTCGCTTCTCTACTGAAGCCACTGATGCTGCAGCTGCGCGTTACGCATGGGCTTTAAAGGCTCGAA 150

TGTGGAGCGAAGAGATGACTTCGGTGACTACGAGCTGACGGCGCAATGCGTACCCGAAATTTTCCGAGCTTT

His Leu Ala Phe Ser Thr Glu Ala Thr Asp Ala Ala Ala Leu Arg Met Gly Phe Lys Lys Ala Arg Lys

AGACGAGGATGGCGGTGTGAAAGTGGGCTGGAGGACAGCCCGCATTCACCAACAGATGTGAGCGCGTTTCGAC 225

TCTGCTCTACCGCCACACTTTTCACCCGACCTCCGCTCGGCTAAGTGGTTGCTACACTCGCGGCAAGCTG

Asp Glu Asp Gly Gly Val Lys Val Gly Leu Glu Ala Glu Pro Asp Ser Pro Thr Asp Val Ser Val Ser Thr

GCCAGTAGTAGAAGAAGCTGTGCGGCGAGCCATGAGCTCCACACAGCCACTTTGGCTCACACAGGACCATCC 300

CGGTCAATCATCTCTTCAGCAGCAGCGGTCGGTACTCGAGGTGTGCGGTGAACCGAGTGTGCTCTGGTAGG

Sac I

Pro Val Val Glu Lys Lys Leu Val Pro Pro Ala Met Ser Ser Thr Gln Pro Leu Trp Leu Thr Gln His Pro

TGTACAGACCTGTGGGCTTTGACCCGAAGATTGTGGTTGGGTCGGAGGAGCTGGAGGAAATCGGTGAA 375

ACACTGTCTGGACAGCCCGCAACGTTCTAACACCCACCAACCGGAGCTCTCGACCTCTTTACGCCACTT

Val Thr Asp Leu Ser Gly Phe Ala Pro Lys Ile Val Val Val Gly Gly Ala Gly Gly Asn Ala Val Asn

ACTCAAGGATAGCGTCCGATACGATGCTGTGATCCCGAACCACCAAACTTGTCAACATGTCAAAATGAGCGCACCTC 825

TGACTTCTATCGCAGCTATGCTACGAACACTAGGCGTTGGTTTGAACAAGTTGACAGTTTACTCGCGGTGGAG

Leu Lys Asp Ser Val Asp Thr Met Leu Val Ile Pro Asp Gln Asn Leu Phe Asn Met Ser Asn Glu Arg Thr Ser

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Sau3A I

BstH II

Pst I

Bsp I

CAACATGATCGCGCGCGCTTGCAGGCTGTGGAGTTTCTTTTGAACACGAGTGTCTACGACTTACGACGAC 450

GTTGTACTAGCGCGCGCGGACGTCCACACACCTCAAGAACAAACGTTGTGCTACGAGTCTGTAATGCGTGTG

Asn Met Ile Ala Arg Gly Leu Gln Gly Val Glu Phe Leu Val Cys Asn Thr Asp Ala Gln His Leu Arg Thr Thr

GCTGACGGAGAACCGCTTCAGATGGCTCTGAAATTGACTGGAGGACTGGGCTGTGGCGCTAACCCCGAAGTTGC 525

CGACTGCTCTTGGCGCAAGTCTACCGAGGACTTAACTGACCTCTCACCCGACACCGCGATTGGGGCTTCAACC

Leu Thr Glu Asn Arg Val Gln Met Ala Pro Glu Leu Thr Gly Leu Gly Cys Gly Ala Asn Pro Glu Val Gly

CCGAGAGCGGAGAGCGCGGATTTGAGCGGCTTTCAGGCTGCAAAACATGATGTTTGTACTGC 800

GGCTCTCCGCGCTCTCCGCGCTAACTACTCTAAACCTCCGCAAGTCCACGTTTGTACTACAAACAATGACG

Arg Glu Ala Ala Glu Ala Ile Asp Glu Ile Leu Glu Arg Val Gln Gly Ala Asn Met Met Phe Val Thr Ala

GGGTATGGTGGGGAACAGGTACAGGTGCAGCACCGCTATTGCTCAGGCTGCCCTTAGATGCTGGTATCCTCAC 675

CCCATACCCACCGCTTGTCCATGTCCAGCTGTGGGCGAGTAACGAGTCCGACGGAATCTACGACCATAGGAGTG

Gly Met Gly Gly Thr Gly Thr Gly Ala Ala Pro Val Ile Ala Gln Ala Ala Leu Asp Ala Gly Ile Leu Thr

Hind III

Slu I

CGTAGCTGTGTTACTAAGCGTTTCGGTTTGGGGAACAAACCGTGCAGGCTTTCGGGCAACAGGCTTCGCTGA 750

GCATCGACAGCAATGATTCGCAAGGCCAAACTCCCTTTGTCGACGTTTCGAACGCCGTGTTCCGGAGCGACT

Val Ala Val Val Thr Lys Pro Phe Arg Phe Glu Gly Asn Asn Arg Ala Lys Leu Ala Gln Gly Leu Ala Glu

Sau3A I

Taq I

Alf III

ACTCAAGGATAGCGTCCGATACGATGCTGTGATCCCGAACCACCAAACTTGTCAACATGTCAAAATGAGCGCACCTC 825

TGACTTCTATCGCAGCTATGCTACGAACACTAGGCGTTGGTTTGAACAAGTTGACAGTTTACTCGCGGTGGAG

Leu Lys Asp Ser Val Asp Thr Met Leu Val Ile Pro Asp Gln Asn Leu Phe Asn Met Ser Asn Glu Arg Thr Ser

FtsZ-m2 consensus2 Map.MPD (1 > 1423) Site and Sequence

TTGGCCAGTATCAAAACCGTAAGCAGGGGAATGACACCTAATGACGTGATTGCTCAAGAAATCTTACAAATTGAA 1350
AACCGGTATAGTTTCGCATTTCGTCCTTACTGTGGATTACTGCGACTAACGAGTTCTTTAGAGATGTTAACTT
Cia I
Taq I
Sau3A I
GTGGCATCGATGCTCTCCACGCCCGCGCGCTGCTGATCGGATTGGTATTATACGGACTGCTTCACTACTAGT 1423
CACCGTAGCTACAGAGGTGCTGGGCGCGCAGGACTAGCTTAACCAATAATATGCTGACGAAGTATGAATCAA

FtsZ-m2 consensus2 Map.MPD (1 > 1423) Site and Sequence

GTTCATGGACCGCATTCAGATCGCGACAATGTCTTCTGGACGGTGTCAAGAACATTTCCGATTGTGATGAT 900
CAACTACCTGGCGTAAGTCTTACCGCTTTACACGAAGACCTGCCACAGTTCTTGAAGCCTAAACTACCACTA
Leu Met Asp Ala Phe Arg Met Ala Asp Asn Val Leu Leu Asp Gly Val Lys Asn Ile Ser Asp Leu Met Val Met
GCCTGGGCTCATTAACTTGAATTTGGGATGTTCAATCGGTGATGCAAAATATGGGAAACGCTATGATGGGAAG 975
CGACCCCGAGTAATTTGGAACCTGAAACGCTTACAAAGTTAGCCAGTACGTTTATACCTTTGGGATACTACCTTC
Pro Gly Leu Ile Asn Leu Asp Phe Ala Asp Val Gin Ser Val Met Gin Asn Met Gly Asn Ala Met Met Gly Ser
TGGAGAGCGCCGATCGAGAGATCGGGCTCTCGCTGCTGAAGTGCATTGGCGAACCTCTTCTGGGTGATAT 1050
ACCTCTCGGGCTACCTCTCTTAGCCCCGAGACGACGACGACTTCTACGTAACCGCTTGGGAGAACCCACCTATA
Gly Glu Ala Asp Gly Glu Asn Arg Ala Leu Arg Ala Glu Asp Ala Leu Ala Asn Pro Leu Leu Gly Asp Ile
Taq I
Sau3A I
TTCGATTAAAGGACGCCAAGGCGATGATCGTTAATATACCGGAGGCTCCGACCTGACGCTATTTGAAGTTGATGA 1125
AAGCTAATTCCTCGGGTTCCCGTACTAGCAATTAATAGTCCCTCCGAGGCTGGACTGCGATAAACTTCACTACT
Ser Ile Lys Asp Ala Lys Gly Met Ile Val Asn Ile Thr Gly Ser Asp Leu Thr Leu Phe Glu Val Asp Glu
Psp I
Sau3A I
Taq I
GGCTGCTGAGCGGTGACCGGGAATTCATGATGATCCACACGCCAACATCATCTTCGGTTCCGACCTTCGACGACTC 1200
CCGACGACTCGCACACTCCGCCCTTGAATCTAGGTGTCGGTGTGTAGTAGAAGCAAGCTGGAAGCTGCTGAG
Ala Ala Glu Arg Val Thr Arg Glu Leu Asp Asp Pro His Ala Asn Ile Ile Phe Gly Ser Thr Phe Asp Ser
Ala III
Mlu I
GCTGGGCGCAAGCTACCGCTCTCCGTGTTGCCACTGGTATTGCCGACCCCGACAAAGTTATAGAACCGTGATG 1275
CGACCCCGCTTCGATCGCAGAGGCGCACCAACGGTGACCAATAACGGCTGGGGCTGTTCAATATCTTCGGCACTAC
Leu Gly Gly Lys Leu Arg Val Ser Val Ala Thr Gly Ile Ala Asp Pro Asp Lys Leu

	Source Organism (organelle)	GenBank Accession No.
SEQ ID NO: 11	<i>Agrobacterium tumefaciens</i>	O30992
SEQ ID NO: 12	<i>Sinorhizobium meliloti</i>	P30327
SEQ ID NO: 13	<i>Bartonella clarridgeiae</i>	AAD31718
SEQ ID NO: 14	<i>Rickettsia prowazekii</i>	Q9ZCQ3
SEQ ID NO: 15	<i>Caulobacter crescentus</i>	P52976
SEQ ID NO: 16	<i>Cyanidioschyzon merolae</i> (mt)	BAA85115
SEQ ID NO: 4	<i>Phytophthora infestans</i> -mt2	this invention
SEQ ID NO: 17	<i>Mallomonas splendens</i> (mt)	AAF35432
SEQ ID NO: 2	<i>Phytophthora infestans</i> -mt1	this invention
SEQ ID NO: 18	<i>Gentiana lutea</i> (cp)	T51088
SEQ ID NO: 19	<i>Nicotiana tabacum</i> (cp, 2-1)	T51087
SEQ ID NO: 20	<i>Arabidopsis thaliana</i> (cp,2-1)	T49028
SEQ ID NO: 21	<i>Physcomitrella patens</i> (cp, 1)	T51089
SEQ ID NO: 22	<i>Physcomitrella patens</i> (cp, 2)	T51090
SEQ ID NO: 23	<i>Guillardia theta</i> (cp)	CAB40398
SEQ ID NO: 24	<i>Mallomonas splendens</i> (cp)	AAF35433
SEQ ID NO: 25	<i>Anabaena</i> PCC7120	CAA83241
SEQ ID NO: 26	<i>Synechocystis</i> PCC6803	P73456
SEQ ID NO: 27	<i>Arabidopsis thaliana</i> (cp,1-1)	Q42545
SEQ ID NO: 28	<i>Pisum sativum</i> (cp)	T06774
SEQ ID NO: 29	<i>Nicotiana tabacum</i> (cp,1-3)	CAB89287
SEQ ID NO: 30	<i>Nicotiana tabacum</i> (cp,1)	CAB41987
SEQ ID NO: 31	<i>Nicotiana tabacum</i> (cp,1-1)	CAB89286
SEQ ID NO: 32	<i>Nicotiana tabacum</i> (cp,2)	AAF23770

Bacterial FtsZ

1

50

SEQ ID NO: 11	PRITVFGVGGGGGNAVNMMITVGLQGVDFVVANTDAQALTMT..KADRVIQLG VNVTEGL
SEQ ID NO: 12	PRITVFGVGGGGGNAVNMMITAGLQGVDFVVANTDAQALTMT..KAERIIQMGVAVTEGL
SEQ ID NO: 13	PRITVFGVGGGGGNAVNMMINAGLQGVDFVVANTDAQALAMS..KAERV IQLGA VTEGL
SEQ ID NO: 14	PTITVFGVGGAGSNAVNMMIHANLQGANFVVANTDAQSLEHS..LCINKIQLGVSTTRGL
SEQ ID NO: 15	PRIVVFGVGGAGGNAVNMMIEAGLEGVEFVVANTDAQQLQFA..KTDRRIQLGVQITQGL

Mitochondrial FtsZ

SEQ ID NO: 16	PRIMVVG VGGAGGNAVNMMIASSLP GVEFLVANTDAQALKMS..LCPNRIQLGASLTEGL
SEQ ID NO: 4	PKIVVVG VGGAGGNAVNMMIARGLQGVFLVCNTDAQHLRTT..LTENRVQMAPELTGGL
SEQ ID NO: 17	PKICVFGVGGGGCNAVNMMIARKLSGVEFVCANTDAQHLSTC..LTENKLQLGKESTQGL
SEQ ID NO: 2	AS.....QLEGVEFIVANTDCQALGRS..LAPHKITL GKDITKGL

Chloroplast FtsZ

SEQ ID NO: 18	AKIKVVG VGGGGSNAVNRMIESAMKGVEFWIVNTDVQAIKMSPVYLENRLQIGQELTRGL
SEQ ID NO: 19	AKIKVVG VGGGGSNAVNRMIESSMKGVEFWIVNTDIQAMRMSPVAAEQRLPIGQELTRGL
SEQ ID NO: 20	ARIKVIG VGGGGSNAVNRMIESEMSGVEFWIVNTDIQAMRMSPVLPDNRLQIGKELTRGL
SEQ ID NO: 21	AKIKVIG VGGGGSNAVNRMLESEM QGVEFWIVNTDAQAMALSPVPAQNRLQIGQKLTRGL
SEQ ID NO: 22	AKIKVIG VGGGGSNAVNRMLESEM QGVEFWIVNTDAQAMALSPVPAQNRLQIGQKLTRGL
SEQ ID NO: 23	CVIKVIG VGGGGNAVNRMVG.GVEGVEFWSINTDAQALSRS..LAPNTCNIGAKLTRGL
SEQ ID NO: 24GVELWVVNTDAQALSRS..SAKRRLNIGKVL SRGL
SEQ ID NO: 25	ANIKVIG VGGGGNAVNRMIESDVSGVEFWSINTDAQALTLA..GAPSRQLIGQKLTRGL
SEQ ID NO: 26	AKIKVIG VGGGGCNAVNRMIASGVTGIDFWAINTDSQALTNT..NAPDCIQIGQKLTRGL
SEQ ID NO: 27	ARIKVIG VGGGGNAVNRMISGLQSVDFY AINTDSQALLQFSA..ENPLQIGELLTRGL
SEQ ID NO: 28	AKIKVIG VGGGGNAVNRMIGSGLQGVDFY AINTDAQALLHSAA..ENPIKIGELLTRGL
SEQ ID NO: 29	AKIKVIG VGGGGNAVNRMIGSGLQGVDFY AINTDAQALLQSAA..ENPLQIGELLTRGL
SEQ ID NO: 30	AKIKVIG VGGGGNAVNRMIGSGLQGVDFY AINTDAQALLQSAA..ENPLQIGELLTRGL
SEQ ID NO: 31	AKIKVVG VGGGGNAVNRMIGSGLQGVDFYAVNTDAQALLQSTV..ENPIQIGELLTRGL
SEQ ID NO: 32	AKIKVVG VGGGGNAVNRMIGSGLQGVDFYAVNTDAQALLQSTV..ENPIQIGELLTRGL

FIG. 2

<u>Bacterial FtsZ</u>	60	110
SEQ ID NO: 11	GAGSQPEVGRAAAEECID E I I D H L N G T H M C F V T A G M G G G T G T G A A P V V A Q A A R N K G I L T V	
SEQ ID NO: 12	GAGSQPEVGRAAAEECID E I I D H L Q G T H M C F V T A G M G G G T G T G A A P I V A Q A A R N K G I L T V	
SEQ ID NO: 13	GAGALPEVGRAAADECID E I I D H L A D S H M V F I T A G M G G G T G T G A A P V V A N A A R E K G I L T V	
SEQ ID NO: 14	GAGASPEVGALAAQES E N E I R S S L E N S N M V F I T A G M G G G T G T G S A P I I A R I A K E L G I L T V	
SEQ ID NO: 15	GAGAHPEVGMSAAEES F P E I G E H L D G A H M V F I T A G M G G G T G T G A A P I I A K C A R E R G I L T V	
<u>Mitochondrial FtsZ</u>		
SEQ ID NO: 16	GAGARPDIGRAAAEEAYETL K R E F R G V H L L F V T A G M G G G T G T G A A P I I A R A A A E L G C L T V	
SEQ ID NO: 4	GCGANPEVGREAAEAAID E I L E R V Q G A N M M F V T A G M G G G T G T G A A P V I A Q A A L D A G I L T V	
SEQ ID NO: 17	GCGANPESGRRAAEESKEE I A R Y I A D A N M V F I T A G M G G G T G T G A A P V V A E V C M E K D I L T V	
SEQ ID NO: 2	GAGSKPELGKRSAEQ Q K V D I Q R M L Q D S N M L F I T G M G G G T C T G A A P V V A S V A R E L G I L T V	
<u>Chloroplast FtsZ</u>		
SEQ ID NO: 18	GAGGNPDIGMNAAKESKEA I E E A V Y G A D M V F V T A G M G G G T G T G G A P V I A G I A K S M G I L T V	
SEQ ID NO: 19	GAGGNPDIGMNAANESKQ A I E E A V Y G A D M V F V T A G M G G G T G T G A A P I I A G T A K S M G I L T V	
SEQ ID NO: 20	GAGGNPEIGMNAARESKEV I E E A L Y G S D M V F V T A G M G G G T G T G A A P V I A G I A K A M G I L T V	
SEQ ID NO: 21	GAGGNPEIGCSAAEESKAMVEEALRGAD M V F V T A G M G G G T G S G A A P I I A G V A K Q L G I L T V	
SEQ ID NO: 22	GAGGNPEIGCSAAEESKAMVEEALRGAD M V F V T A G M G G G T G S G A A P I I A G V A K Q L G I L T V	
SEQ ID NO: 23	GAGGNPEIGRKAEEESRD L I A E A V S A G D L V F V T A G M G G G T G S G A A P I V A E V A K E M G C L T V	
SEQ ID NO: 24	GAGGNPAIGKAAEESR E E I M A V V K N A D L V F V T A G M G G G T G S G A A P V V A E C A K E A G A L T V	
SEQ ID NO: 25	GAGGNPAIGQKAAEESR D E I A T A L E G A D L V F I T A G M G G G T G T G A A P I V A E V A K E M G A L T V	
SEQ ID NO: 26	GAGGNPAIGQKAAEESR D E I A R S L E G T D L V F I T A G M G G G T G T G A A P I V A E V A K E M G C L T V	
SEQ ID NO: 27	GTGGNPLLGEQAAEESK D A I A N A L K G S D L V F I T A G M G G G T G S G A A P V V A Q I S K D A G Y L T V	
SEQ ID NO: 28	GTGGNPLLGEQAAEESK E A I A N A L K G S D L V F I T A G M G G G T G S G A A P V V A Q I S K E A G Y L T V	
SEQ ID NO: 29	GTGGNPLLGEQAAEESK E A I A N S L K G S D M V F I T A G M G G G T G S G A A P V V A Q I A K E A G Y L T V	
SEQ ID NO: 30	GTGGNPLLGEQAAEESK E A I A N S L K G S D M V F I T A G M G G G T G S G A A P V V A Q I A K E A G Y L T V	
SEQ ID NO: 31	GTGGNPLLGEQAAEESK E H I A N A L K G S D M V F I T A G M G G G T G S G A A P V V A Q I A K E A G Y L T V	
SEQ ID NO: 32	GTGGNPLLGEQAAEESK E H I A N A L K G S D M V F I T A G M G G G T G S G A A P V V A Q I A K E A G Y L T V	
<u>Bacterial FtsZ</u>	120	170
SEQ ID NO: 11	GVVTKPFHFEGGRRMRLAEQ G I E E L Q K S V D T L I V I P N Q N L F R I A N D K T T F A D A F A M A D Q V	
SEQ ID NO: 12	GVVTKPFHFEGGRRMRIADQ G I S D L Q K S V D T L I V I P N Q N L F R I A N D K T T F A D A F A M A D Q V	
SEQ ID NO: 13	GVVTKPFQFEGARRMKTAEAG I E E L Q K S V D T L I V I P N Q N L F R I A N E K T T F S D A F A M A D Q V	
SEQ ID NO: 14	GVVTKPFHFEGGHRMKTADKGL I E L Q Q F V D T L I V I P N Q N L F R I A N E Q T T F A D A F K M A D D V	
SEQ ID NO: 15	GVVTKPFHFEGRRHRLADSG I Q E L Q R Y V D T L I V I P N Q N L F R V A N E R T T F A E A F G M A D Q V	
<u>Mitochondrial FtsZ</u>		
SEQ ID NO: 16	AVVTKPFHFEGMIRMKTAEQ G I V E L T E H V D T M L V I P N Q N L F K V A S P R T S F L D A F R L A D H V	
SEQ ID NO: 4	AVVTKPFRFEGNNRAKLAAQGLAELKDSVD T M L V I P N Q N L F N M S N E R T S L M D A F R M A D N V	
SEQ ID NO: 17	AVVTKPFSFEGKHRARLANEG I R S L E D R V D T L I I P N Q N I F K L I N A S T S M A D A F L A D D I	
SEQ ID NO: 2	GVVSTPFRSEGNRRLANAGVKELAKYVD T L I V V P N Q N L L A L A D K S T T M L E A F R Y A D D V	
<u>Chloroplast FtsZ</u>		
SEQ ID NO: 18	GIVTTPFSFEGRRRAVQAQEG I A A L R D N V D T L I V I P N D K L L T A V S P S T P V T E A F N L A D D I	
SEQ ID NO: 19	GIVTTPFSFEGRRRAVQAQEG I A A L R E N V D T L I V I P N D K L L T A V S P S T P V T E A F N L A D D I	
SEQ ID NO: 20	GIATTPFSFEGRRRTVQAQEG L A S L R D N V D T L I V I P N D K L L T A V S Q S T P V T E A F N L A D D I	
SEQ ID NO: 21	GIVTTPFAFEGRRRAVQAHEG I A A L K N N V D T L I T I P N N K L L T A V A Q S T P V T E A F N L A D D I	
SEQ ID NO: 22	GIVTTPFAFEGRRRSVQAHEG I A A L K N N V D T L I T I P N N K L L T A V A Q S T P V T E A F N L A D D I	
SEQ ID NO: 23	GVVTKPFAFEGKRMRQQA D A I L N L R N K V D T L I V V S N D K L L Q I V P D N T P L Q D A F S V A D D I	
SEQ ID NO: 24	GVVTKPFGFEGKRMRQQA R N A I L E M K D K V D T L I V V S N D K L L K I V P D N T P L T E A F L V A D D I	
SEQ ID NO: 25	GVVTRPFFVFEGRRTSQAEG I E G L K S R V D T L I I P N N K L L E V I P E Q T P V Q E A F R Y A D D V	
SEQ ID NO: 26	GIVTRPFTFEGRRRAKQAEEG I A L K S R V D T L I V I P N N Q L L S V I P A E T P L Q E A F R V A D D I	
SEQ ID NO: 27	GVVTPFSFEGRRKSLQALEA I E K L Q K N V D T L I V I P N D R L L D I A D E Q T P L Q D A F L L A D D V	
SEQ ID NO: 28	GVVTPFSFEGRRKSLQALEA I E K L Q K N V D T L I V I P N D R L L D I A D E Q M P L Q D A F R L A D D V	
SEQ ID NO: 29	GVVTPFSFEGRRKRSVQALEA I E K L Q K N V D T L I V I P N D R L L D I A D E Q T P L Q D A F L L A D D V	
SEQ ID NO: 30	GVVTPFSFEGRRKRSVQALEA I E K L Q K N V D T L I V I P N D R L L D I A D E Q T P L Q D A F L L A D D V	
SEQ ID NO: 31	GVVTPFSFEGRRKRS L Q A L E A I E K L Q K N V D T L I V I P N D R L L D I A D E Q T P L Q N A F L L A D D V	
SEQ ID NO: 32	GVVTPFSFEGRRKRS L Q A L E A I E K L Q K N V D T L I V I P N D R L L D I A D E Q T P L Q N A F L L A D D V	

FIG. 2

<u>Bacterial FtsZ</u>	180	230
SEQ ID NO: 11	LYSGVACITDLMVKEGLINLDFADVRSVMREMARPMGTGE...	ASGPARAMQAAEAAI
SEQ ID NO: 12	LYSGVACITDLMVKEGLINLDFADVRSVMREMGMMGTGE...	ASGEGRAMAAEAAI
SEQ ID NO: 13	LYSGVASITDLMIKEGLINLDFADVRSVMHEMGMMGTGE...	ASGDGRALAAEAAI
SEQ ID NO: 14	LHAGVRGVTDLMIMPGLINLDFADIKAVMSEMKGMMGTGE...	DSGEDRAIKAAESAI
SEQ ID NO: 15	LHSGVRSITDLMVLPGLINLDFADVRTVMTEMGMMGTGE...	GTAEDRALMAAQNAI
<u>Mitochondrial FtsZ</u>		
SEQ ID NO: 16	LYSGVRSITDLMTPGLINLDFADVRSVVREMGMMGSGEVEMEAGNEERAIRASEAAI	
SEQ ID NO: 4	LLDGVKNISDLMVMPGLINLDFADVQSVQMNGNAMMGSGEAD...	GENRALRAAEDAL
SEQ ID NO: 17	LLAGVKSITDLMVRPGLINLDFADVRTVMSGMGHAIMGTGQAE...	GEDRAIRAANDAL
SEQ ID NO: 2	LLEGVKGVTDLIVRPGLINL.....	
<u>Chloroplast FtsZ</u>		
SEQ ID NO: 18	LRQGVRGISDIITIPGLVNVDFAVRAIMANAGSSLMGIGT...	ATGKTRARDAALNAI
SEQ ID NO: 19	LRQGVRGISDIITIPGLVNVDFAVRAIMANAGSSLMGIGT...	ATGKTRARDAALNAI
SEQ ID NO: 20	LRQGVRGISDIITIPGLVNVDFAVRAIMANAGSSLMGIGT...	ATGKSRARDAALNAI
SEQ ID NO: 21	LRQGVRGISDIITIPGLVNVDFAVRAIMANAGSSLMGIGT...	ATGKSRAREAAALSAI
SEQ ID NO: 22	LRQGVRGISDIITIPGLVNVDFAVRAIMANAGSSLMGIGT...	ATGKSKAREAAALSAI
SEQ ID NO: 23	LRQGVVGISEIIVRPGLINVDFAVRSVMADAGSALMGIGT...	GSGKTRAQDAAVAAI
SEQ ID NO: 24	LRQGVVGITEIIVKPGLVNVDFAVVRTIMGNAGTALMGIGH...	GKGKNRAKDAALSAI
SEQ ID NO: 25	LRQGVQGISDIITIPGLVNVDFAVRAVMADAGSALMGIGV...	SSGKSRAREAAIAAI
SEQ ID NO: 26	LRQGVQGISDIITIPGLVNVDFAVRAVMADAGSALMGIGV...	GSGKSRAREAAATAAI
SEQ ID NO: 27	LRQGVQGISDIITIPGLVNVDFAVKAVMKDSGTAMLGVG...	SSSKNRAEEAAEQAT
SEQ ID NO: 28	LRQGVQGISDIITIPGLVNVDFAVKAVMKDSGTAMLGVG...	SSGKNRAEEAAEQAT
SEQ ID NO: 29	LRQGVQGISDIITIPGLVNVDFAVKAVMKDSGTAMLGVG...	SSSKNRAEEAAEQAT
SEQ ID NO: 30	LRQGVQGISDIITIPGLVNVDFAVKAVMKDSGTAMLGVG...	SSSKNRAEEAAEQAT
SEQ ID NO: 31	LCQGVQGISDIITIPGLVNVDFAVKAIMKDSGTAMLGVG...	SSSRNRAEEAAEQAT
SEQ ID NO: 32	LCQGVQGISDIITIPGLVNVDFAVKAIMKDSGTAMLGVG...	SSSRNRAEEAAEQAT
<u>Bacterial FtsZ</u>	240	290
SEQ ID NO: 11	ANPLLD.ETSMKGAQGLLISITGGRDLTLFEVDEAATRIREEVDP.	DANIILGATFDEAL
SEQ ID NO: 12	ANPLLD.ETSMKGAQGLLISITGGRDLTLFEVDEAATRIREEVDP.	DANIILGATFDEEL
SEQ ID NO: 13	ANPLLD.DTSMRGARGLLISITGGRDMTLFEVDEAANRIREEVDA.	DANVIFGAIDDES
SEQ ID NO: 14	SNPLLD.HSSMCGARGVLINITGGPDMTLFEVDNAANRIREEVDNIDANI	IFGSTFNPEL
SEQ ID NO: 15	ANPLLD.EVSLKGAKAVLVNVTGGMDMTLFEVDEAANAISDQVDP.	EANIIFGAAFDP
<u>Mitochondrial FtsZ</u>		
SEQ ID NO: 16	CNPLLD.ETSLRGARGVLVNITGGTDMTLFEIDAAANRIREQVDP.	DANIIFGSFAFDASM
SEQ ID NO: 4	ANPLLG.DISIKDAKMIVNITGGSDDLTLFEVDEAAERTRELD	PHANIIFGSTFDDSL
SEQ ID NO: 17	NNPLLGDFSRSAGMLVNITGGKDLTLFEVDAAAQRITSEI	EDEDANVIFGSSFDES
SEQ ID NO: 2	
<u>Chloroplast FtsZ</u>		
SEQ ID NO: 18	QSPLLD..IGIERATGIVWNITGGSDDLTLFEVNAAA	AEVIYDLVDP.SANLIFGAVVDPSL
SEQ ID NO: 19	QSPLLD..IGIERATGIVWNITGGSDDLTLFEVNAAA	AEVIYDLVDP.SANLIFGAVIDPSI
SEQ ID NO: 20	QSPLLD..IGIERATGIVWNITGGSDDLTLFEVNAAA	AEVIYDLVDP.TANLIFGAVVDPAL
SEQ ID NO: 21	QSPLLD..VGIERATGIVWNITGGSDDLTLFEVNAAA	AEVIYDLVDP.NANLIFGAVVDEAL
SEQ ID NO: 22	QSPLLD..VGIERATGIVWNITGGSDDLTLFEVNAAA	AEVIYDLVDP.NANLIFGAVVDEAL
SEQ ID NO: 23	SSPLLD..FPIEKARGIVFNITGGQDMTLHEINSAA	AEVIYEAVDS.NANIIFGALVDDNM
SEQ ID NO: 24	SSPLLD..FPITRAKGIVFNIVGSDMSLQEINAAA	AEVIYENVVQ.DANIIFGAMVDDKM
SEQ ID NO: 25	SSPLLE..CSIEGARGVFNITGGSDDLTLHEVNAAA	ETIYEVVDP.NANIIFGAVIDDRL
SEQ ID NO: 26	SSPLLE..SSIQAGKGVFNVTGGTDLTLHEVNAAA	EIIYEVVDA.DANIIFGAVIDDRL
SEQ ID NO: 27	LAPLIG..SSIQSATGVVYNITGGKDITLQEVNRVS	QVVVTSADP.SANIIFGAVVDDRY
SEQ ID NO: 28	LAPLIG..SSIQSATGVVYNITGGKDITLQEVNRVS	QVVVTSADP.SANIIFGAVVDDRY
SEQ ID NO: 29	LAPLIG..SSIQSATGVVYNITGGKDITLQEVNRVS	QVVVTSADP.SANIIFGAVVDERY
SEQ ID NO: 30	LAPLIG..SSIQSATGVVYNITGGKDITLQEVNRVS	QVVVTSADP.SANIIFGAVVDERY
SEQ ID NO: 31	LAPLIG..LSIQSATGVVYNITGGKDITLQEVN	KVSQVVVTSADP.SANIIFGAVVDERY
SEQ ID NO: 32	LAPLIG..SSIQSATGDVYNITGGKDITLQEVN	KVSQVVVTSADP.SANIIFGAVVDERY

FIG. 2

Bacterial FtsZ

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SEQ ID NO: 11	E.GLIRVSVVATGI
SEQ ID NO: 12	E.GLIRVSVVATGI
SEQ ID NO: 13	E.GVIRVSVVATGI
SEQ ID NO: 14	K.GIIRVSVVATGI
SEQ ID NO: 15	E.GVIRVSVVATGM

Mitochondrial FtsZ

SEQ ID NO: 16	Q.GRLRVSVLATGI
SEQ ID NO: 4	G.GKLRVSVVATGI
SEQ ID NO: 17	Q.GSIRVSIVATGI
SEQ ID NO: 2

Chloroplast FtsZ

SEQ ID NO: 18	C.GQVSITLIATGF
SEQ ID NO: 19	S.GQVSITLIATGF
SEQ ID NO: 20	S.GQVSITLIATGF
SEQ ID NO: 21	H.GQVSITLIATGF
SEQ ID NO: 22	H.DQISITLIATGF
SEQ ID NO: 23	EN.EISITVVATGF
SEQ ID NO: 24	TSGEVSITVLATGF
SEQ ID NO: 25	Q.GEVKITVIATGF
SEQ ID NO: 26	Q.GEMKITVIATGF
SEQ ID NO: 27	.TGEIHVTIIATGF
SEQ ID NO: 28	.TGEIHVTIIATGF
SEQ ID NO: 29	.NGEIHVTIIATGF
SEQ ID NO: 30	.NGEIHVTIIATGF
SEQ ID NO: 31	.NGEIQVTIIATGF
SEQ ID NO: 32	.NGEIQVTIIATGF

FIG. 2

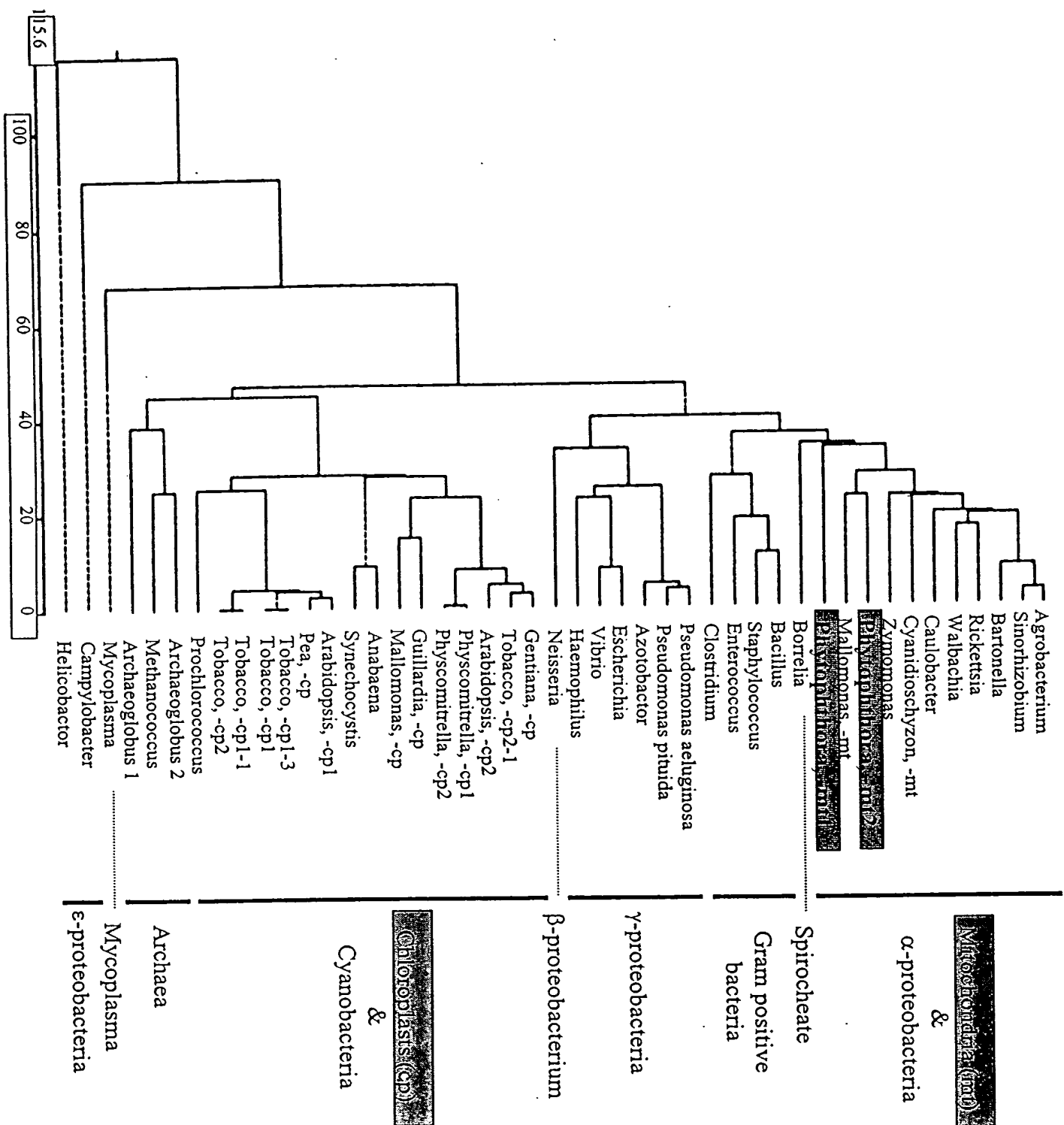


FIG. 3